RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _____10/781, 659_____

Source: _____IFWO_____

Date Processed by STIC: _____07/26/2005_____

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/781,659

DATE: 07/26/2005
TIME: 09:31:21

Input Set : **N:\Crf3\RULE60\10781659.raw**
Output Set: **N:\CRF4\07262005\J781659.raw**

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 1 <110> APPLICANT: ITOH, Kyogo et al.
 2 <120> TITLE OF INVENTION: NOVEL TUMOR ANTIGEN PROTEIN SART-3 AND TUMOR ANTIGEN
 3       PEPTIDES THEREOF
 4 <130> FILE REFERENCE: 0020-4817P
 5 <140> CURRENT APPLICATION NUMBER: US/10/781,659
 6 <141> CURRENT FILING DATE: 2004-02-20
 7 <150> PRIOR APPLICATION NUMBER: US/09/763,985
 8 <151> PRIOR FILING DATE: 2001-02-28
 9 <160> NUMBER OF SEQ ID NOS: 64
10 <170> SOFTWARE: PatentIn version 3.1
12 <210> SEQ ID NO: 1
13 <211> LENGTH: 3798
14 <212> TYPE: DNA
15 <213> ORGANISM: Homo sapiens
16 <220> FEATURE:
17 <221> NAME/KEY: CDS
18 <222> LOCATION: (12)..(2900)
19 <223> OTHER INFORMATION:
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24       gct gag tcc aag gct ggg ccc aag gct gac gga gag gag gat gag gtt      98
25       Ala Glu Ser Lys Ala Gly Pro Lys Ala Asp Gly Glu Glu Asp Glu Val
26          15                  20                  25
27       aag gcg gct agg aca agg aga aag gtg tta tcg cgg gct gtg gcc gct      146
28       Lys Ala Ala Arg Thr Arg Arg Lys Val Leu Ser Arg Ala Val Ala Ala
29       30                  35                  40                  45
30       gcg aca tac aag acc atg ggg cca gcg tgg gat cag cag gag gaa ggc      194
31       Ala Thr Tyr Lys Thr Met Gly Pro Ala Trp Asp Gln Gln Glu Glu Gly
32                       50                  55                  60
33       gtg agc gag agc gat ggg gat gag tac gcc atg gct tcc tcc gcg gag      242
34       Val Ser Glu Ser Asp Gly Asp Glu Tyr Ala Met Ala Ser Ser Ala Glu
35                       65                  70                  75
36       agc tcc ccc ggg gag tac gag tgg gaa tat gac gaa gag gag gag aaa      290
37       Ser Ser Pro Gly Glu Tyr Glu Trp Glu Tyr Asp Glu Glu Glu Glu Lys
38                       80                  85                  90
39       aac cag ctg gag att gag aga ctg gag gag cag ttg tct atc aac gtc      338
40       Asn Gln Leu Glu Ile Glu Arg Leu Glu Glu Gln Leu Ser Ile Asn Val
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42       tat gac tac aac tgc cat gtg gac ttg atc aga ctg ctc agg ctg gaa      386
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44       110                 115                 120                 125
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7/26/05

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46      Gly Glu Leu Thr Lys Val Arg Met Ala Arg Gln Lys Met Ser Glu Ile
47                  130                 135                 140
48      ttt ccc ttg act gaa gag ctc tgg ctg gag tgg ctg cat gac gag atc      482
49      Phe Pro Leu Thr Glu Glu Leu Trp Leu Glu Trp Leu His Asp Glu Ile
50                  145                 150                 155
51      agc atg gcc cag gat ggc ctg gac aga gag cac gtg tat gac ctc ttt      530
52      Ser Met Ala Gln Asp Gly Leu Asp Arg Glu His Val Tyr Asp Leu Phe
53                  160                 165                 170
54      gag aaa gcc gtg aag gat tac att tgt cct aac att tgg cta gag tat      578
55      Glu Lys Ala Val Lys Asp Tyr Ile Cys Pro Asn Ile Trp Leu Glu Tyr
56          175                 180                 185
57      ggc cag tac tca gtt ggt ggg att ggt cag aaa ggt ggc ctt gag aaa      626
58      Gly Gln Tyr Ser Val Gly Gly Ile Gly Gln Lys Gly Gly Leu Glu Lys
59      190                 195                 200                 205
60      gtt cgc tcc gtg ttt gaa agg gct ctc tcg tct gtt ggt tta cat atg      674
61      Val Arg Ser Val Phe Glu Arg Ala Leu Ser Ser Val Gly Leu His Met
62                  210                 215                 220
63      acc aaa gga ctc gcc ctc tgg gag gct tac cga gag ttt gaa agt gcg      722
64      Thr Lys Gly Leu Ala Leu Trp Glu Ala Tyr Arg Glu Phe Glu Ser Ala
65                  225                 230                 235
66      att gtg gaa gct gct cgg ctt gag aaa gtc cac agt ctt ttc cgg cga      770
67      Ile Val Glu Ala Ala Arg Leu Glu Lys Val His Ser Leu Phe Arg Arg
68                  240                 245                 250
69      cag ttg gcg atc cca ctc tat gat atg gag gcc aca ttt gca gag tat      818
70      Gln Leu Ala Ile Pro Leu Tyr Asp Met Glu Ala Thr Phe Ala Glu Tyr
71          255                 260                 265
72      gaa gaa tgg tca gaa gac cca ata cca gag tca gta att cag aac tat      866
73      Glu Glu Trp Ser Glu Asp Pro Ile Pro Glu Ser Val Ile Gln Asn Tyr
74      270                 275                 280                 285
75      aac aaa gca cta cag cag ctg gag aaa tat aaa ccc tat gaa gaa gca      914
76      Asn Lys Ala Leu Gln Gln Leu Glu Lys Tyr Lys Pro Tyr Glu Glu Ala
77                  290                 295                 300
78      ctg ttg cag gca gag gca cca agg ctg gca gaa tat caa gca tat atc      962
79      Leu Leu Gln Ala Glu Ala Pro Arg Leu Ala Glu Tyr Gln Ala Tyr Ile
80                  305                 310                 315
81      gat ttt gag atg aaa att ggc gat cct gct cgc att cag ttg atc ttt     1010
82      Asp Phe Glu Met Lys Ile Gly Asp Pro Ala Arg Ile Gln Leu Ile Phe
83                  320                 325                 330
84      gag cgc gcc ctg gtc gag aac tgc ctt gtc cca gac tta tgg atc cgt     1058
85      Glu Arg Ala Leu Val Glu Asn Cys Leu Val Pro Asp Leu Trp Ile Arg
86          335                 340                 345
87      tac agt cag tac cta gat cga caa ctg aaa gta aag gat ttg gtt tta     1106
88      Tyr Ser Gln Tyr Leu Asp Arg Gln Leu Lys Val Lys Asp Leu Val Leu
89      350                 355                 360                 365
90      tct gta cat aac cgc gct att aga aac tgc ccc tgg aca gtt gcc tta     1154
91      Ser Val His Asn Arg Ala Ile Arg Asn Cys Pro Trp Thr Val Ala Leu
92                  370                 375                 380
93      tgg agt cgg tac ctc ttg gcc atg gag aga cat gga gtt gat cat caa     1202
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 94     Trp Ser Arg Tyr Leu Leu Ala Met Glu Arg His Gly Val Asp His Gln
 95                     385                 390                 395
 96     gta att tct gta acc ttc gag aaa gct ttg aat gcc ggc ttc atc cag    1250
 97     Val Ile Ser Val Thr Phe Glu Lys Ala Leu Asn Ala Gly Phe Ile Gln
 98                     400                 405                 410
 99     gcc act gat tat gtg gag att tgg cag gca tac ctt gat tac ctg agg    1298
100     Ala Thr Asp Tyr Val Glu Ile Trp Gln Ala Tyr Leu Asp Tyr Leu Arg
101                 415                 420                 425
102     aga agg gtt gat ttc aaa caa gac tcc agt aaa gag ctg gag gag ttg    1346
103     Arg Arg Val Asp Phe Lys Gln Asp Ser Ser Lys Glu Leu Glu Glu Leu
104         430                 435                 440                 445
105     agg gcc gcc ttt act cgt gcc ttg gag tat ctg aag cag gag gtg gaa    1394
106     Arg Ala Ala Phe Thr Arg Ala Leu Glu Tyr Leu Lys Gln Glu Val Glu
107                     450                 455                 460
108     gag cgt ttc aat gag agt ggt gat cca agc tgc gtg att atg cag aac    1442
109     Glu Arg Phe Asn Glu Ser Gly Asp Pro Ser Cys Val Ile Met Gln Asn
110                     465                 470                 475
111     tgg gct agg att gag gct cga ctg tgc aat aac atg cag aaa gct cgg    1490
112     Trp Ala Arg Ile Glu Ala Arg Leu Cys Asn Asn Met Gln Lys Ala Arg
113                 480                 485                 490
114     gaa ctc tgg gat agc atc atg acc aga gga aat gcc aag tac gcc aac    1538
115     Glu Leu Trp Asp Ser Ile Met Thr Arg Gly Asn Ala Lys Tyr Ala Asn
116         495                 500                 505
117     atg tgg cta gag tat tac aac ctg gaa aga gct cat ggt gac acc cag    1586
118     Met Trp Leu Glu Tyr Tyr Asn Leu Glu Arg Ala His Gly Asp Thr Gln
119     510                 515                 520                 525
120     cac tgc cgg aag gct ctg cac cgg gcc gtc cag tgc acc agt gac tac    1634
121     His Cys Arg Lys Ala Leu His Arg Ala Val Gln Cys Thr Ser Asp Tyr
122                 530                 535                 540
123     cca gag cac gtc tgc gaa gtg tta ctc acc atg gag agg aca gaa ggt    1682
124     Pro Glu His Val Cys Glu Val Leu Leu Thr Met Glu Arg Thr Glu Gly
125                 545                 550                 555
126     tct tta gaa gat tgg gat ata gct gtt cag aaa act gaa acc cga tta    1730
127     Ser Leu Glu Asp Trp Asp Ile Ala Val Gln Lys Thr Glu Thr Arg Leu
128                 560                 565                 570
129     gct cgt gtc aat gag cag aga atg aag gct gca gag aag gaa gca gcc    1778
130     Ala Arg Val Asn Glu Gln Arg Met Lys Ala Ala Glu Lys Glu Ala Ala
131         575                 580                 585
132     ctt gtg cag caa gaa gaa gaa aag gct gaa caa cgg aaa aga gct cgg    1826
133     Leu Val Gln Gln Glu Glu Glu Lys Ala Glu Gln Arg Lys Arg Ala Arg
134     590                 595                 600                 605
135     gct gag aag aaa gcg tta aaa aag aag aaa aag atc aga ggc cca gag    1874
136     Ala Glu Lys Lys Ala Leu Lys Lys Lys Lys Ile Arg Gly Pro Glu
137                 610                 615                 620
138     aag cgc gga gca gat gag gac gat gag aaa gag tgg ggc gat gat gaa    1922
139     Lys Arg Gly Ala Asp Glu Asp Asp Glu Lys Glu Trp Gly Asp Asp Glu
140                 625                 630                 635
141     gaa gag cag cct tcc aaa cgc aga agg gtc gag aac agc atc cct gca    1970
142     Glu Glu Gln Pro Ser Lys Arg Arg Arg Val Glu Asn Ser Ile Pro Ala
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143              640                 645                 650
144       gct gga gaa aca caa aat gta gaa gta gca gca ggg ccc gct ggg aaa        2018
145       Ala Gly Glu Thr Gln Asn Val Glu Val Ala Ala Gly Pro Ala Gly Lys
146           655                 660                 665
147       tgt gct gcc gta gat gtg gag ccc cct tcg aag cag aag gag aag gca        2066
148       Cys Ala Ala Val Asp Val Glu Pro Pro Ser Lys Gln Lys Glu Lys Ala
149       670                 675                 680                 685
150       gcc tcc ctg aag agg gac atg ccc aag gtg ctg cac gac agc agc aag        2114
151       Ala Ser Leu Lys Arg Asp Met Pro Lys Val Leu His Asp Ser Ser Lys
152               690                 695                 700
153       gac agc atc acc gtc ttt gtc agc aac ctg ccc tac agc atg cag gag        2162
154       Asp Ser Ile Thr Val Phe Val Ser Asn Leu Pro Tyr Ser Met Gln Glu
155               705                 710                 715
156       ccg gac acg aag ctc agg cca ctc ttc gag gcc tgt ggg gag gtg gtc        2210
157       Pro Asp Thr Lys Leu Arg Pro Leu Phe Glu Ala Cys Gly Glu Val Val
158               720                 725                 730
159       cag atc cga ccc atc ttc agc aac cgt ggg gat ttc cga ggt tac tgc        2258
160       Gln Ile Arg Pro Ile Phe Ser Asn Arg Gly Asp Phe Arg Gly Tyr Cys
161           735                 740                 745
162       tac gtg gag ttt aaa gaa gag aaa tca gcc ctt cag gca ctg gag atg        2306
163       Tyr Val Glu Phe Lys Glu Glu Lys Ser Ala Leu Gln Ala Leu Glu Met
164       750                 755                 760                 765
165       gac cgg aaa agt gta gaa ggg agg cca atg ttt gtt tcc ccc tgt gtg        2354
166       Asp Arg Lys Ser Val Glu Gly Arg Pro Met Phe Val Ser Pro Cys Val
167               770                 775                 780
168       gat aag agc aaa aac ccc gat ttt aag gtg ttc agg tac agc act tcc        2402
169       Asp Lys Ser Lys Asn Pro Asp Phe Lys Val Phe Arg Tyr Ser Thr Ser
170               785                 790                 795
171       cta gag aaa cac aag ctg ttc atc tca ggc ctg cct ttc tcc tgt act        2450
172       Leu Glu Lys His Lys Leu Phe Ile Ser Gly Leu Pro Phe Ser Cys Thr
173               800                 805                 810
174       aaa gag gaa cta gaa gaa atc tgt aag gct cat ggc acc gtg aag gac        2498
175       Lys Glu Glu Leu Glu Glu Ile Cys Lys Ala His Gly Thr Val Lys Asp
176           815                 820                 825
177       ctc agg ctg gtc acc aac cgg gct ggc aaa cca aag ggc ctg gcc tac        2546
178       Leu Arg Leu Val Thr Asn Arg Ala Gly Lys Pro Lys Gly Leu Ala Tyr
179       830                 835                 840                 845
180       gtg gag tat gaa aat gaa tcc cag gcg tcg cag gct gtg atg aag atg        2594
181       Val Glu Tyr Glu Asn Glu Ser Gln Ala Ser Gln Ala Val Met Lys Met
182               850                 855                 860
183       gac ggc atg act atc aaa gag aac atc atc aaa gtg gca atc agc aac        2642
184       Asp Gly Met Thr Ile Lys Glu Asn Ile Ile Lys Val Ala Ile Ser Asn
185               865                 870                 875
186       cct cct cag agg aaa gtt cca gag aag cca gag acc agg aag gca cca        2690
187       Pro Pro Gln Arg Lys Val Pro Glu Lys Pro Glu Thr Arg Lys Ala Pro
188               880                 885                 890
189       ggt ggc ccc atg ctt ttg ccg cag aca tac gga gcg agg ggg aag gga        2738
190       Gly Gly Pro Met Leu Leu Pro Gln Thr Tyr Gly Ala Arg Gly Lys Gly
191           895                 900                 905
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192        agg acg cag ctg tct cta ctg cct cgt gcc ctg cag cgc cca agt gct        2786
193        Arg Thr Gln Leu Ser Leu Leu Pro Arg Ala Leu Gln Arg Pro Ser Ala
194        910                 915                 920                 925
195        gca gct cct cag gct gag aac ggc cct gcc gcg gct cct gca gtt gcc        2834
196        Ala Ala Pro Gln Ala Glu Asn Gly Pro Ala Ala Ala Pro Ala Val Ala
197                        930                 935                 940
198        gcc cca gca gcc acc gag gca ccc aag atg tcc aat gcc gat ttt gcc        2882
199        Ala Pro Ala Ala Thr Glu Ala Pro Lys Met Ser Asn Ala Asp Phe Ala
200                        945                 950                 955
201        aag ctg ttt ctg aga aag tgaacgggac gctgggagac aggaaatgcc              2930
202        Lys Leu Phe Leu Arg Lys
203                960
204        ttacttcact ctggcccggc ggacctccca ccacccagca gtgcactggg gatggacagg     2990
205        cctggtgtgc tgcgtgctcg caaccacaga tggctcctcg gctttagaca gaaaggggaa     3050
206        ggggttctaa gtcaagagcc tttcagtgct ccctcatatt gagggcagtg gcagaaaagt     3110
207        gaccactctg caggctgggc ccaggatgtg gtgtcctgag atagttttgt atcttaaaga     3170
208        ctgaggcaca gaagcgaaac gagaacacac tgtttttgag acacagttgt ccaaatgttt     3230
209        ctggccagct ccggcccctt tttgtatgac acttctcttc caccctgcac agcacatgtg     3290
210        cccgtcattc tttaatttt aaaagatgaa atggcagatg ctagtaattc acagaatggc      3350
211        ctcttgtggg ggtgggtctg agggaagtca gctataaaac atttgctgga gttttgttca     3410
212        atggggctgt gcattttat attatgtgtt tgtaaatgac atgtcagccc ttgtttcatg      3470
213        tttcctaaaa gcagaatatt tgcaacattt gttttgtata ggaattattt gtgccacctg     3530
214        ctgtggactg ttttctttgc ctagtgacta gtgacctgtg ttgtctaaac atgagtttca     3590
215        gccctttggt tttgtttaat accatgtcaa atgcaaactt caattctccc catttagctt     3650
216        tattaaactg acgttctctt caaaacttct tgctgaatgg tactcagatg tgcattcaca     3710
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221 <211>  LENGTH: 963
222 <212>  TYPE: PRT
223 <213>  ORGANISM: Homo sapiens
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230                        35                  40                  45
231        Lys Thr Met Gly Pro Ala Trp Asp Gln Gln Glu Glu Gly Val Ser Glu
232                50                  55                  60
233        Ser Asp Gly Asp Glu Tyr Ala Met Ala Ser Ser Ala Glu Ser Ser Pro
234        65                  70                  75                  80
235        Gly Glu Tyr Glu Trp Glu Tyr Asp Glu Glu Glu Glu Lys Asn Gln Leu
236                        85                  90                  95
237        Glu Ile Glu Arg Leu Glu Glu Gln Leu Ser Ile Asn Val Tyr Asp Tyr
238                        100                 105                 110
239        Asn Cys His Val Asp Leu Ile Arg Leu Leu Arg Leu Glu Gly Glu Leu
240                        115                 120                 125
241        Thr Lys Val Arg Met Ala Arg Gln Lys Met Ser Glu Ile Phe Pro Leu
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 07/26/2005
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Input Set : N:\Crf3\RULE60\10781659.raw
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:53; Xaa Pos. 2,10
Seq#:54; Xaa Pos. 2,10
Seq#:55; Xaa Pos. 2,9
Seq#:56; Xaa Pos. 2,9
Seq#:57; Xaa Pos. 2,10
Seq#:58; Xaa Pos. 2,9
Seq#:59; Xaa Pos. 2,9
Seq#:60; Xaa Pos. 2,9
Seq#:61; Xaa Pos. 2,9
Seq#:62; Xaa Pos. 2,9
Seq#:63; Xaa Pos. 2,9
Seq#:64; Xaa Pos. 2,9

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Input Set : N:\Crf3\RULE60\10781659.raw
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L:753 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:756 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:53
L:759 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:53
L:760 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53 after pos.:0
L:769 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:772 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:54
L:775 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:54
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Input Set : **N:\Crf3\RULE60\10781659.raw**
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